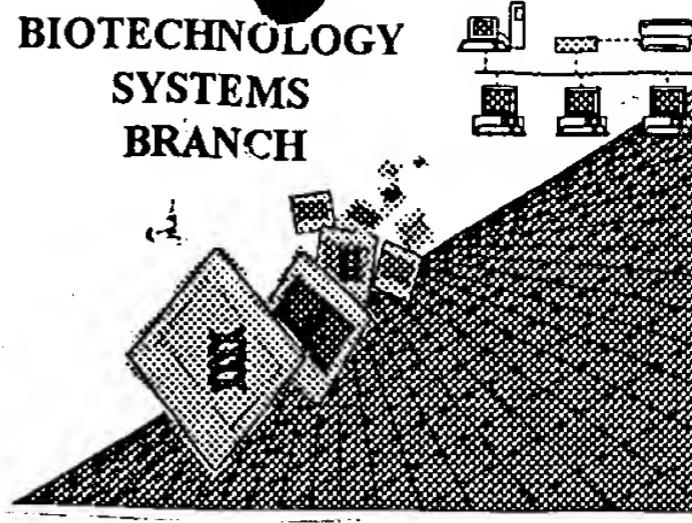


0590
0831

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/841,157

Source: O/PE

Date Processed by STIC: 10/11/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/841,157

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <u>1-44</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/841,157

DATE: 10/11/2001
TIME: 10:40:08

Input Set : A:\US09841157SEQLIST.txt
Output Set: N:\CRF3\10112001\I841157.raw

3 <110> APPLICANT: Taitec Co., Ltd.
W--> 4 <120> TITLE OF INVENTION: Method for identifying an organism by its genotype
C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/841,157
C--> 5 <141> CURRENT FILING DATE: 2001-04-25
E--> 5 <160> NUMBER OF SEQ ID:
W--> 0 <130> FILE REFERENCE:
E--> 5 <160> NUMBER OF SEQ ID NOS:

ERRORRED SEQUENCES

W--> 6 <210> SEQ ID NO: 1
7 <211> LENGTH: 204
8 <212> TYPE: DNA
W--> 9 <211> LENGTH: unknown
W--> 10 <213> ORGANISM:
E--> 10 <400> SEQUENCE: 0
11 tgctacgtct cttccgatgc tgtcttcgc tgctgagggt gacgatcccg caaaagcggc 60
12 ctttgactcc ctgcaaggcct cagcgaccga atatatcggt tatgcgtggg cgatggttgt 120
13 tgtcattgtc ggcgcaacta tcggtatcaa gctgtttaag aaattcacct cgaaagcaag 180
14 ctgataaacc gatagaattc aagg 204
55 <210> SEQ ID NO: 8
E--> 56 <211>12
57 <212> TYPE: DNA
58 <211> LENGTH: unknown
W--> 59 <213> ORGANISM:
W--> 59 <400> SEQUENCE: 8
E--> 60 aaatttaaat tt 12
61 <210> SEQ ID NO: 9
62 <211> LENGTH: 12
63 <212> TYPE: DNA
W--> 64 <211> LENGTH: unknown
W--> 65 <213> ORGANISM:
W--> 65 <400> SEQUENCE: 9
E--> 66 aattaattaa tt
187 <210> SEQ ID NO: 30
188 <211> LENGTH: 12
189 <212> TYPE: DNA
W--> 190 <211> LENGTH: unknown
W--> 191 <213> ORGANISM:
W--> 191 <400> SEQUENCE: 30
E--> 192 gatcacctcc tta 13)
193 <210> SEQ ID NO: 31
194 <211> LENGTH: 12
195 <212> TYPE: DNA
W--> 196 <211> LENGTH: unknown
W--> 197 <213> ORGANISM:

Does Not Comply
Corrected Diskette Needed

See following pages

Many errors

*Please consult
Sequence Rules*

09/84/157

2

delete

SEQUENCE LISTING

<110> Taitec Co., Ltd.

<120> Method for identifying an organism by its genotype

<160> *mandatory response needed (44 shown)*

insert these
mandatory
numbers
remove
identifiers
and responses

<210>1

<211>204

<212>DNA

<213> *<211>Unknown* see item 11 on Error summary sheet

<400>1

tgctacgtct cttccgatgc tgtcttcgc tgctgagggt gacgatcccc caaaagcgcc 60
cttgactcc ctgcaagcct cagcgaccga atatatcggt tatgcgtggg cgatggtgt 120
tgtcattgtc ggcgcaacta tcggtatcaa gctgtttaag aaattcacct cgaaagcaag 180
ctgataaacc gatagaattc aagg 204

<210>2

<211>286

<212>DNA

<211>Unknown

<400>2

attggcgccg tggcaacgat tgcccggtgcg caaggcggcg taatgcgtca tgtcaaaccg 60
cacggcatgt tgtacaacca ggccggcgaaa gaagcacaac tggcagacgc catcgccaga 120
gcggtatacg cttgcgatcc agcattgatt ctcgtcgggc tggcgggaag cgagctgatt 180
cgtcaggca agcaatatgg tctgacaacg cgcgaggaag tggccgttat tcgcggttat 240
caggctgacg gctcgctggt gccgcgaagc cagtcaggcg cggtga 286

<210>3

<211>12

<212>DNA

<211>Unknown

<400>3

cagtcaggac gt 12

<210>4

<211>12

<212>DNA

<211>Unknown

<400>4

agaacgcgcc tg 12

<210>5

<211>12

<212>DNA

<211>Unknown

<400>5

cgtcgctatt aa 12

<210>6

<211>12

<212>DNA

<211>Unknown

<400>6

cagggcgccgt ac 12

<210>7

<211>12

<212>DNA

<211>Unknown

<400>7

aaaaaaaaaa ad 12

<210>8

<211>12

<212>DNA

Please ensure
all <211> responses
=
match actual
number of bases

09/841,157 3

<211>unknown
<400>8
aaatttaaat tt 12
<210>9
<211>12
<212>DNA
<211>unknown
<400>9
aattaattaa tt
<210>10
<211>12
<212>DNA
<211>unknown
<400>10
acgacgacga cg 12
<210>11
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<212>DNA
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<400>11
atatatatat at 12
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<212>DNA
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cccccccccc cc 12
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ccggccggcc gg 12
<210>14
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<212>DNA
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<210>16
<211>12
<212>DNA
<211>unknown
<400>16
gagagagaga ga 12
<210>17
<211>12
<212>DNA
<211>unknown
<400>17
ggccggccgg cc 12

12 ← insert

09/841,157 4

<210>18
<211>12
<212>DNA
(211)unknown
<400>18
ttttttttt tt 12
<210>19
<211>12
<212>DNA
(211)unknown
<400>19
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(211)unknown
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gctaaaadaa aa 12
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<400>26
caattctaca ac 12
<210>27
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<212>DNA

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<211>unknown
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<210>28
<211>12
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tataattata at 12
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<211>unknown
<400>29
attataatta ta 12
<210>30
<211>12
<212>DNA
<211>unknown
<400>30
gatcacctcc tta 13 () delete parentheses
<210>31
<211>12 / 13
<212>DNA
<211>unknown
<400>31
taaggagggtg atc 13
<210>32
<211>12
<212>DNA
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<400>32
cccacccacc ca 12
<210>33
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<400>35
cagaaaaacag ctatgacgtt ctcac 25
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<400>36
ggcgatatcc ctgaaa 16

09/841,157

6

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<400>39

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<210>40

<211>18 17

<212>DNA

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<400>40

FITC-cagggaaaca gctatgac 18 17

<210>41

<211>31

<212>DNA

<211>unknown

<400>41

FITC-tgctacgtct cttccgatgc tgtctttcgc t 31

<210>42

<211>31

delete space

<212>DNA

<211>unknown

<400>42

cy3-tgctacgtct cttccgatgc tgtctttcgc t 31

<210>43

<211>12

<212>DNA

<211>unknown

<400>43

HEX-gaacctcccc ac 12

<210>44

<211>12

<212>DNA

<211>unknown

<400>44

TAM-Tgctgctgct gc 12

delete

use lower-case letters

show bases only - no dashes or extraneous material

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

(JMS)